



SEQUENCE LISTING

<110> Monteiro, et al.
<120> Method of Controlling the Binding of Calmyrin to Presenilin
<130> 4115-161
<150> 60/210,939
<151> 2000-06-11
<160> 29
<170> PatentIn version 3.1
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<211> 448
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<213> Homo sapiens
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Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
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Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
35 40 45

Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
50 55 60

Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
65 70 75 80

Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
85 90 95

Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
100 105 110

Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
115 120 125

Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
130 135 140

Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
145 150 155 160

Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
165 170 175

Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
 180 185 190
 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
 195 200 205
 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
 210 215 220
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
 225 230 235 240
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
 245 250 255
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
 260 265 270
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
 325 330 335
 Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
 340 345 350
 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
 370 375 380
 Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
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Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
 435 440 445

<210> 2
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<400> 2

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Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Thr Val Glu Ser Ser
 35 40 45

Leu Arg Ala Gln Val Pro Phe Glu Gln Ile Leu Ser Leu Pro Glu Leu
 50 55 60

Lys Ala Asn Pro Phe Lys Glu Arg Ile Cys Arg Val Phe Ser Thr Ser
 65 70 75 80

Pro Ala Lys Asp Ser Leu Ser Phe Glu Asp Phe Leu Asp Leu Leu Ser
 85 90 95

Val Phe Ser Asp Thr Ala Thr Pro Asp Ile Lys Ser His Tyr Ala Phe
 100 105 110

Arg Ile Phe Asp Phe Asp Asp Asp Gly Thr Leu Asn Arg Glu Asp Leu
 115 120 125

Ser Arg Leu Val Asn Cys Leu Thr Gly Glu Gly Glu Asp Thr Arg Leu
 130 135 140

Ser Ala Ser Glu Met Lys Gln Leu Ile Asp Asn Ile Leu Glu Glu Ser
 145 150 155 160

Asp Ile Asp Arg Asp Gly Thr Ile Asn Leu Ser Glu Phe Gln His Val
 165 170 175

Ile Ser Arg Ser Pro Asp Phe Ala Ser Ser Phe Lys Ile Val Leu
 180 185 190

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Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
 35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
 50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
 65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
 85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
 100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
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450 455 460

Phe Tyr Ile
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gccacagagc taaagtgact tttcccaagg tcgcccagcg aggacgtggg acttctcaga     180
cgtcaggaga gtgatgtgag ggagctgtgt gaccatagaa agtgacgtgt taaaaaccag     240
cgctgccctc tttgaaagcc agggagcatc attcatttag cctgctgaga agaagaaacc     300
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gggctatgct cacattcatg gcctctgaca gcgaggaaga agtgtgtgat gagcggacgt     420
ccctaattgc ggccgagagc cccacgccgc gctcctgccg ggagggcagg cagggcccag     480
aggatggaga gaatactgcc cagtggagaa gccaggagaa cgaggaggac ggtgaggagg     540
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tgaccctcaa atacggagcg aagcatgtga tcatgctgtt tgtgcctgtc actctgtgca     660
tgatcgtggt ggtagccacc atcaagtctg tgcgcttcta cacagagaag aatggacagc     720
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tctacaagta ccgctgttac aagttcatcc atggctgggt gatcatgtct tcaactgatgc     900
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gcgtgaagct tggcctcggg gacttcatct tctacagtgt gctggtgggc aaggcggctg    1500
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tgtgtctgac cctcctgctg cttgctgtgt tcaagaaggc gctgcccgcc ctccccatct    1620
ccatcacgtt cgggctcatc ttttacttct ccacggacaa cctggtgcgg ccgttcatgg    1680
acaccctggc ctcccatcag ctctacatct gagggacatg gtgtgccaca ggctgcaagc    1740
tgcagggaat tttcattgga tgcagttgta tagttttaca ctctagtgcc atatattttt    1800
aagacttttc tttccttaaa aaataaagta cgtgtttact tggtagaggag gaggcagaac    1860

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Calmyrin.ST25.txt

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cagctctttg gtgccagctg tttcatcacc agactttggc tcccgctttg gggagcgcct 1920
cgcttcacgg acaggaagca cagcagggtt atccagatga actgagaagg tcagattagg 1980
gtggggagaa gagcatccgg catgagggct gagatgccca aagagtgtgc tcgggagtgg 2040
cccctggcac ctgggtgctc tggctggaga ggaaaagcca gttccctacg aggagtgttc 2100
ccaatgcttt gtccatgatg tccttggtat tttattnccy ttanaaactg antcctnttn 2160
ttnttdcggc agtcacmctn ctgggragtg gcttaatagt aanatcaata aanagntgag 2220
tcctnttaga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2280
aaaaa 2285
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ttgacgttcc tgacgaagca ggagatcctc ctagcccaca ggcggttttg tgagctgctt 180
ccccaggagc agcggaccgt ggagtcgtca cttcgggcac aagtgcctt cgagcagatt 240
ctcagccttc cagagctcaa ggccaacccc ttcaaggagc gaatctgcag ggtcttctcc 300
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gatgacggaa ccttgaacag agaagacctg agccggctgg tgaactgcct cacgggagag 480
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gagtctgaca ttgacagga tggaaccatc aacctctctg agttccagca cgtcatctcc 600
cgttctccag actttgccag ctctttaaag attgtcctgt gacagcagcc ccagcgtgtg 660
tcttggcacc ctgtccaaga acctttctac tgctgagctg tggccaaggt caagcctgtg 720
ttgccagtgc gggccaagct ggcccagcct ggagctggcg ctgtgcagcc tcaccccggg 780
caggggcggc cctcgttgtc agggcctctc ctactgctg ttgtcattgc tccgtttgtg 840
tttgactaa tcagtaataa aggttttagaa gtttgaccct aaaaa 885
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<213> Homo sapiens
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20 25 30

Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu Ala Gln Arg Arg
35 40 45

Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr Glu Arg Glu Ser
50 55 60

Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe Ser Glu Glu Trp
65 70 75 80

Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg Ser Thr Pro Glu
85 90 95

Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile Leu Ala Gly Glu
100 105 110

Asp Pro Glu Glu Arg Gly Val Lys
115 120

<210> 28
<211> 101
<212> PRT
<213> Homo sapiens

<400> 28

Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met
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20 25 30

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35 40 45

Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp Pro Glu Met Glu
50 55 60

Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr Pro Glu Val Phe
65 70 75 80

Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu Glu Glu Glu
85 90 95

Glu Arg Gly Val Lys
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<210> 29
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<212> PRT
<213> Artificial Sequence

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<223> Synthetic Construct

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